UNIVERSITY OF PENNSYLVANIA HEALTH SYSTEM

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Response to the Mayberg and Evans "Re-analysis"

October 3, 2007

Fred Duchardt, Esq.

Dear Mr. Duchardt:

Frankly I was somewhat perturbed by the tone and innuendos contained in Drs. Evans and Mayberg's recent salvo (admittedly not at the level of Mr. Whitworth in his emails). I have at every stage represented exactly what I did and everything I said, in the reports and testimony, is true and correct. They were the ones who said that I used different methods for calculating the control and Ms. Montgomery's values, and asked for all individual data to prove their point. I sent them all the data I had as soon as I had it, and with every shipment I explained what was in the files. Some of the "multiple" mailings they now complain about were done to help accommodate them and save them time and effort. I ended every mailing with an invitation to ask any questions they had, and they sometimes took me up on the offer. Usually, however, they went ahead making their assumptions and produced a variety of legitimate and illegitimate graphs and numbers. They did reproduce my graphs when they followed the procedures I articulated in my report, and I never did what they said I did in the other calculations and graphs, so I don't see their relevance to the discussion and I am concerned that some of them serve no other purpose than to obfuscate the issue. Perhaps a bullet form presentation can help clear the smoke:

- I routinely receive R/WB values, such as are presented in the original report (Figure 4), from the PET Center where they are calculated the same way for controls and for Ms. Montgomery (or anyone else): "counts-per pixel" (cpp) for each region is divided by cpp for the whole brain. I also receive metabolic rates for each region and the whole brain, quantified in physiologic units (ml/100 g/minute). Since Montgomery's study was quantified with cpp, I used the R/WB values.
- Evans and Mayberg said that I used different methods for the two data sets, specifically that I used cpp for Ms. Montgomery but the average of 36 regions for the control sample. Hence their request for my "raw data". While the original cpp data used by the PET Center to calculate the R/WB values would have been ideal for proving their claim, I suggested and they seem to have accepted that they could find out whether I did that, and what would have been the effect of having done that, if I send them all the data I have.

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- As I explained, I used the same method for both Ms. Montgomery and the controls. The PET Center provides me with R/WB ratios based on cpp and I get also raw metabolic rates, but not the count rates used to calculate the R/WB ratios. The PET Center had these data for Ms. Montgomery, and I forwarded them as soon as I got them, but for the old normative data it had to initiate a long process of "thawing" (which they hope to complete this week).
- In the meanwhile I offered all the data I do have, which included the R/WB and the raw metabolic rates in physiological units in each region. This could have allowed them to test their hypothesis and they accepted and used these data. I find it hard toi believe that they did not know what they were analyzing. The cpp and metabolic rate, as well as R/WB values, have distinctively different values. I also offered normative data on the current scanner with cpp information, and they thought this was relevant. Their complaint that I flooded them with irrelevant information is disingenuous.
- With the data they have, they could have proved their hypothesis and they didn't. They could have shown that when one uses the average of 36 regions for the controls it reproduces the values I showed in Figure 4, while if one uses the correct volume whole brain as the denominator one gets values that look like Montgomery's (there is no dispute that Montgomery's data were calculated correctly using the global whole-brain cpp). Rather, the data for controls are nearly identical when we use the raw metabolic rates in physiologic units normalized to whole-brain volume (Figure 1 of my September 28, 2007 report) and when we use cpp (Figure 4 of my original report). On the other hand, the values of the controls when the wrong method of averaging 35 or 36 regions is used are similar but not the same for controls.
- They claim that because the results for controls using the wrong method of averaging the 36 or 35 regions are similar to the data I showed for controls, therefore I must have used that wrong method. The similarity of results does not prove that I used the wrong method. It only proves that for controls it matters very little which method is used. So their hypothesis has already been rejected by the data.
- The only time when they get Ms. Montgomery's data to be within the normal range is when they use the wrong method of averaging 35 or 36 regions for the denominator of R/WB (what they call gray matter, but it is NOT gray matter) both for the controls and for Ms. Montgomery. Since I did not use the wrong method, and the values are different when the wrong method is used, they have failed to support their conjecture that I used the wrong method in the controls.
- The cpp data we are in process of extracting are very unlikely to help their case. This is not surprising. The comparability of R/WB data based on cpp versus metabolic rates has been investigated extensively in our Center and elsewhere, and the general conclusion is that they are quite equivalent. Therefore, their request for the cpp data is no longer relevant for proving that I used different methods for calculating Montgomery and control data. They showed no evidence that I did, and what they show indicates that I did not.

Sincerely,

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